

RESULT 13

AAX26588

ID AAX26588 standard; DNA; 2169 BP.

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AC AAX26588;

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DT 16-JUN-1999 (first entry)

XX

DE Nucleotide sequence of murine KCNQ2 (formerly known as (KvLR1).

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KW KCNQ protein; nervous system-specific potassium channel;

KW neuronal excitability; neurotransmitter release; KCNQ modulator;

KW ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;

KW age-associated memory loss; learning deficiency; motor neuron disease;

KW epilepsy; stroke; ss.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT CDS 1..2169

FT /*tag= a

XX

PN WO9907832-A1.

XX

PD 18-FEB-1999.

XX

PF 26-JUN-1998; 98WO-US13276.

XX

PR 12-AUG-1997; 97US-0055599.

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PA (BRIM) BRISTOL-MYERS SQUIBB CO.

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PI Blanar MA, Dworetzky S, Gribkoff VK, Levesque PC;

PI Little WA, Neubauer MG, Yang W;

XX

DR WPI; 1999-190047/16.

DR P-PSDB; AAY01530.

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PT New potassium channels, KCNQ2 and KCNQ3 - may be involved in

PT neurotransmission and neuroprotection, used to treat, e.g. ataxia

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PS Claim 7; Fig 10A-D; 64pp; English.

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CC The present sequence encodes murine KCNQ2/KvLR1. KCNQ proteins are
 CC nervous system-specific potassium channels. In neurons, potassium
 CC channels regulate neuronal excitability, action potential shape
 CC and firing pattern, and neurotransmitter release. KCNQ modulators
 CC may be used to treat disorders such as ataxia, myokymia, seizures,
 CC Alzheimer's disease, Parkinson's disease, age-associated memory
 CC loss, learning deficiencies, motor neuron diseases, epilepsy, and
 CC stroke.

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SQ Sequence 2169 BP; 466 A; 622 C; 635 G; 446 T; 0 other;

Query Match 18.9%; Score 510; DB 20; Length 2169;

Best Local Similarity 58.1%; Pred. No. 1e-139;

Matches 1043; Conservative 0; Mismatches 670; Indels 81; Gaps 5;

Qy 64 GGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTGAGG 123

Db 67 GGCTTCGTGGGGCTGGACCCGCGCGGCCGACTCCACACGCGACGGCGGCTACTCATC 126

Qy 124 GAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCTTAC 183

Db 127 GCGGGCTCCGAGGCCCCAAGCGCGGCAGCGTTTGTAGCAAGCCGCGACGGCGGCGCG 186

Qy 184 ACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTGTAC 243

Db 187 GGAGCCGGGAAGCCCCGAAGCGCAACGCCTTCTACGCAAGCTGCAGAAATTCCTCTAC 246

Qy 244 AACGTGCTGGAGAGACCCCGCGGCTGGGCGTTTCATCTACCACGCTTTCGTTTTCTCCTT 303

Db 247 AACGTGCTAGAGCGGCCCGCGGCTGGGCGTTTCATCTACCACGCCTACGTGTTCTCTTTTA 306
 Qy 304 GTCTTTGGTTGCTTGATTTTGTCACTGTTTCTACCATCCCTGAGCACACAAAATTGGCC 363
 Db 307 GTCTTCTCCTGCCTTGTGCTTCTGTGTTTTCCACCATCAAGGAGTACGAGAAGAGCTCT 366
 Qy 364 TCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTCATC 423
 Db 367 GAGGGGGCCCTCTACATCTTGAAATCGTGACTATCGTGGTATTCGGTGTGAGTACTTT 426
 Qy 424 ATTCGAATCTGGTCTGCGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTGAGG 483
 Db 427 GTGAGGATCTGGGCTGCAGGCTGCTGTTGCCGGTATCGAGGCTGGAGGGGAGGCTCAAG 486
 Qy 484 TTTGTCGAAAAGCCCTTCTGTGTTATAGATACCATGTTCTTATCGCTTCAATAGCAGTT 543
 Db 487 TTTGCCAGGAAGCCGTTCTGTGTGATTGATATCATGGTGCTGATTGCCTCCATTGCTGTG 546
 Qy 544 GTTCTGCAAAAAGCTCAGGTAATATTTTGGCCAGTCTGCACTCAGAAGTCTCCGTTTC 603
 Db 547 CTGGTCTGCTGGTTCCAGGGCAATGTCTTTGCCACATCTGCGCTTCGGAGCTTGGCGTTC 606
 Qy 604 CTACAGATCTCCGCATGGTGCAGATGGACCGAAGGGGAGGCACTTGGAATTAAGGGT 663
 Db 607 TTGCAATCTTGCGGATGATCCGTATGGACCGGAGGGGTGGCACCTGGAAGCTCTTGGGA 666
 Qy 664 TCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTGGTT 723
 Db 667 TCGGTAGTCTACGCTCACAGCAAGGAGCTGGTGACTGCCTGGTACATGGCTTCCTCTGC 726
 Qy 724 CTTATTTTTTCGTCTTTCTTGTCTATCTGGTGGAAAAGGATGCCAATAAGAGTTTCT 783
 Db 727 CTCATCCTGGCCTCATTTCTGGTGTACTTGGCAGAAAAGGGTGAGAATGACCACTTTGAC 786
 Qy 784 ACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACCTATTGGCTATGGAGAC 843
 Db 787 ACCTACGCAGATGCACTCTGGTGGGGTCTGATCACCTGACGACCTATTGGCTACGGGGAC 846
 Qy 844 AAAACTCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGCATT 903
 Db 847 AAGTACCCTCAGACCTGGAACGGGAGGCTGCTGGCAGCGACCTTTACCCTCATTGGTGTG 906
 Qy 904 TCTTTCTTTGCACTTCCTGCGGCACTTCTTGGCTCAGGTTTTCATTAAAGTACAAGAA 963
 Db 907 TCCTTCTTTGCTCTTCTGCTGGCATTTTGGGATCCGGCTTGCCTGAAAGTCAAGAG 966
 Qy 964 CAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTAGTGT 1023
 Db 967 CAGCATCGGCAAAAACACTTTGAGAAACGGCGGAACCTGCGGCAGGTCTGATCCAGTCT 1026
 Qy 1024 GTTGGCGTAGTTACGCAGCTGATGAGAAAT----- 1054
 Db 1027 GCCTGGAGATTCTATGCTACTAACCTCTCACGCACCGACCTGCACTCCACGTGGCAGTAC 1086
 Qy 1055 -----CTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGAC 1098
 Db 1087 TACGAGCGGACAGTCACTGTCCCATGTACAGACTCATCCACCTCTGAACAGCTGGAG 1146
 Qy 1099 ACCTGCAGCCCTACCAAGA-----AAGAACAAGGGGAA 1131
 Db 1147 CTGCTGAGGAATCTCAAGAGCAAATCTGGACTCACCTTCAGGAAGGAGCCACAGCCAGAG 1206
 Qy 1132 GCATCAAGCAGTCAGAAGCTAAGTTTAAAGGAGCGAG---TGCGCATGGCTAGCCCCAGG 1188
 Db 1207 CCATCAACCAAGTCAGAAGGTCAGTTTGAAGATCGTGTCTTCTCCAGCCCCGAGGCATG 1266
 Qy 1189 GGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCAAGCACCGAC 1248
 Db 1267 GCTGCCAAGGGAAAGGGGTCTCCCAGGCCAGACGGTCCGGCGGTCCCCAGTGCAGGAT 1326

Qy	1249	ATCACAGCCGAGGGCAGTCCCACCAAAGTGCGAGAAGAGCTGGAGCTTCAACGACCGGAACC	1308
Db	1327	CAGAGTCTTGATGACAGCCCGAGCAAGGTGCCAAGAGCTGGAGCTTTGGTGACCGCAGC	1386
Qy	1309	CGCTTCGGCCCTCGCTGCGCCTCAAAGTTCTCAGCCAAAACAGTGATAGATGCTGAC	1368
Db	1387	CGCACACGCCAGGCTTTCGCATCAAGGGTGCTGCATCCCGGCAGAATTAGAAGCAAGC	1446
Qy	1369	ACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTG	1428
Db	1447	C---TCCCTGGGGAGGACATCGTAGAGGACAACAAGAGCTGTAAGTGCAGCTTTGTGACT	1503
Qy	1429	GAAGACCTCACCCACCACTTAAACTGTCAATTCGAGCTATCAGAATTATGAAATTCAT	1488
Db	1504	GAAGATCTTACCCCTGGCCTCAAAGTTAGCATCAGAGCTGTGTGTGTTATGCGGTTCTTG	1563
Qy	1489	GTGCAAAACGGAAGTTTTAAGGAAACGTTACGTCCATATGATGTAAAGATGTCATTGAA	1548
Db	1564	GTATCTAAGCGAAAGTTCAAAGAGAGTCTGCGCCCATATGATGTGATGGACGTCATCGAA	1623
Qy	1549	CAATATTCTGCTGGTCACTCTGGACATGTTGTGTAGAATTAAGCCTTCAAACACGTGTT	1608
Db	1624	CAGTACTCGGCTGGACACTTGGATATGTTGTCCGCATCAAGAGCCTGCAGTCCAGAGTG	1683
Qy	1609	GATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACA	1668
Db	1684	GACCAGATTGTGGGGCGGGGCCAACAAATAACGATAAGGA---TCGCACCAAAGGCCCA	1740
Qy	1669	GCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGTGCGGTGGTCAAGGTTGAAAAA	1728
Db	1741	GCGGAAACGAGAGCTGCCGAAGACCCAGCATGATGGGACGGCTTGGGAAGGTGGAGAAA	1800
Qy	1729	CAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAG	1782
Db	1801	CAGGTCTTGTCCATGAAAAAGAGCTCGACTTCTTGGTGAGCATCTATACACAG	1854